



## SEQUENCE LISTING

RECEIVED

MAR 15 2001

TECH CENTER 1600/2900

<110> Parham, Christopher L.  
Moore, Kevin W.  
Murgolo, Nicholas J.  
Bazan, J. Fernando

<120> Human Receptor Proteins; Related Reagents and Methods

<130> DX0804K

<140> 09/265,540

<141> 1999-03-08

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<170> PatentIn Ver. 2.0

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translated amino acid depends on genetic code

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translated amino acid depends on genetic code

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translated amino acid depends on genetic code

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&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1369)

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translated amino acid depends on genetic code

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agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120

gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr
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agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218

Ser	Leu	Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr
15					20						25				

gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266

Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser
30					35					40					45

acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314

Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly
				50					55					60	

gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362

Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu
			65					70					75		

tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410

Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu
		80					85					90			

ggc cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458

Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr
	95					100					105				

aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506

Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser
110					115					120					125

atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554  
 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro  
 130 135 140  
 ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag 602  
 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu  
 145 150 155  
 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650  
 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu  
 160 165 170  
 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698  
 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro  
 175 180 185  
 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746  
 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala  
 190 195 200 205  
 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794  
 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr  
 210 215 220  
 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842  
 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu  
 225 230 235  
 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890  
 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe  
 240 245 250  
 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938  
 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val  
 255 260 265  
 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986  
 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
 270 275 280 285  
 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser  
                             290                            295                            300

cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084

Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
                             305                            310

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tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgct tacaagtcta 1204

gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264

gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324

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                             20                            25                            30

Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met  
                             35                            40                            45

Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
                             50                            55                            60

Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser  
   65                            70                            75                            80

His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu  
                             85                            90                            95

Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg  
                             100                            105                            110

Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
 115 120 125  
 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu  
 130 135 140  
 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly  
 145 150 155 160  
 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala  
 165 170 175  
 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu  
 180 185 190  
 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe  
 195 200 205  
 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val  
 210 215 220  
 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 225 230 235 240  
 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys  
 245 250 255  
 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro  
 260 265 270  
 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg  
 275 280 285  
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 Leu Leu Arg Ala Trp Ile Ser  
 305 310

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Trp	Phe	Leu	Ser	Cys	Trp	Asn	Val	Thr	Ile	Gly	Pro	Pro	Glu	Ser	Ile
			20					25					30		

tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145

Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	Pro
		35					40					45			

ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193

Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	Xaa
	50					55					60				

tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241

Trp	Glu	Lys	Ala	Gly	Ile	Gln	Lys	Val	Lys	Gly	Pro	Phe	Lys	Ser	Asn
65					70					75					80

tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289

Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	Gln
				85					90					95	

gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337

Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	Gly
			100					105					110		

cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385

Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	Thr
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Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	Leu
	130					135					140				

gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481

Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	Gly
145					150					155					160

ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529  
 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
 165 170 175  
 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577  
 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
 180 185 190  
 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625  
 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
 195 200 205  
 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673  
 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
 210 215 220  
 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggt ctgagccgag 724  
 Gln Asn Ser Gly Ala Val Cys  
 225 230  
 gaagctgctg atgtccatgt cagcacttta tggaatccgg tcctccattt tcctgtcccc 784  
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			20					25					30		
Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	Pro
		35					40					45			
Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	Xaa
	50					55					60				
Trp	Glu	Lys	Ala	Gly	Ile	Gln	Lys	Val	Lys	Gly	Pro	Phe	Lys	Ser	Asn
65					70					75					80
Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	Gln
				85					90					95	
Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	Gly
			100					105					110		
Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	Thr
		115					120					125			
Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	Leu
	130					135					140				
Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	Gly
145					150					155					160
Leu	Val	Lys	Tyr	Trp	Phe	His	Ser	Pro	Pro	Ser	Ile	Pro	Ser	Gln	Ile
				165					170					175	
Glu	Glu	Tyr	Leu	Lys	Asp	Pro	Ser	Gln	Pro	Ile	Leu	Glu	Ala	Leu	Asp
			180					185					190		
Lys	Asp	Thr	Ser	Pro	Thr	Asp	Asp	Ala	Trp	Asp	Leu	Val	Ser	Val	Val
		195					200					205			
Ala	Phe	Pro	Ala	Lys	Glu	Gln	Glu	Asp	Val	Pro	Gln	Ser	Thr	Leu	Thr
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Gln	Asn	Ser	Gly	Ala	Val	Cys									
225					230										



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Pro	Gln	His	Pro	Lys	Ile	Arg	Leu	Tyr	Asn	Ala	Glu	Gln	Val	Leu	Ser	35	40	45	
Trp	Glu	Pro	Val	Ala	Leu	Ser	Asn	Ser	Thr	Arg	Pro	Val	Val	Tyr	Arg	50	55	60	
Val	Gln	Phe	Lys	Tyr	Thr	Asp	Ser	Lys	Trp	Phe	Thr	Ala	Asp	Ile	Met	65	70	75	80
Ser	Ile	Gly	Val	Asn	Cys	Thr	Gln	Ile	Thr	Ala	Thr	Glu	Cys	Asp	Phe	85	90	95	
Thr	Ala	Ala	Ser	Pro	Ser	Ala	Gly	Phe	Pro	Met	Asp	Phe	Asn	Val	Thr	100	105	110	
Leu	Arg	Leu	Arg	Ala	Glu	Leu	Gly	Ala	Leu	His	Ser	Ala	Trp	Val	Thr	115	120	125	
Met	Pro	Trp	Phe	Gln	His	Tyr	Arg	Asn	Val	Thr	Val	Gly	Pro	Pro	Glu	130	135	140	
Asn	Ile	Glu	Val	Thr	Pro	Gly	Glu	Gly	Ser	Leu	Ile	Ile	Arg	Phe	Ser	145	150	155	160
Ser	Pro	Phe	Asp	Ile	Ala	Asp	Thr	Ser	Thr	Ala	Phe	Phe	Cys	Tyr	Tyr	165	170	175	
Val	His	Tyr	Trp	Glu	Lys	Gly	Gly	Ile	Gln	Gln	Val	Lys	Gly	Pro	Phe	180	185	190	
Arg	Ser	Asn	Ser	Ile	Ser	Leu	Asp	Asn	Leu	Lys	Pro	Ser	Arg	Val	Tyr	195	200	205	
Cys	Leu	Gln	Val	Gln	Ala	Gln	Leu	Leu	Trp	Asn	Lys	Ser	Asn	Ile	Phe	210	215	220	
Arg	Val	Gly	His	Leu	Ser	Asn	Ile	Ser	Cys	Tyr	Glu	Thr	Met	Ala	Asp	225	230	235	240

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Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
          35          40          45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
          50          55          60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
  65          70          75          80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
          85          90          95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
          100          105          110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
          115          120          125

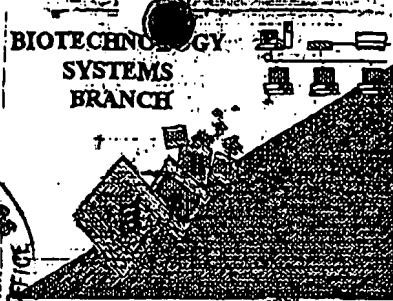
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 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
 165 170 175  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
 180 185 190  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
 195 200 205  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala  
 210 215 220  
 Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly  
 225 230 235 240  
 Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe  
 245 250 255  
 Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His  
 260 265 270  
 Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu  
 275 280 285  
 Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser  
 290 295 300  
 Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly  
 305 310 315 320  
 Gln Gly Pro Gln Ser  
 325

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BIOTECHNOLOGY  
SYSTEMS  
BRANCH

**RAW SEQUENCE LISTING  
ERROR REPORT**



RECEIVED

JAN 10 2001

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,540C

Source: 1643

Date Processed by STIC: 1/2/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/265,540C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8        Skipped Sequences (OLD RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xl) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(III) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences (NEW RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism (NEW RULES)      Sequence(s)        are missing this mandatory field or its response.
- 12        Use of <220>Feature (NEW RULES)      Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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1643

JAN 10 2001

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/265,540CDATE: 01/03/2001  
TIME: 12:23:01

TECH CENTER 1600/2900

Input Seq : A:\804k.app  
Output Seq : N:\CRF3\01022001\I265540C.rawDoes Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Parham, Christel L.  
 2 <110> Moore, Kevin W.  
 3 <110> Burgallo, Nicholas J.  
 4 <110> Lujan, J. Fernando  
 5 <170> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods  
 6 <130> FILE REFERENCE: DX0901K  
 7 <110> CURRENT APPLICATION NUMBER: 09/265,540C  
 8 <111> CURRENT FILING DATE: 1999-03-08  
 9 <160> NUMBER OF SEQ ID NOS: 6  
 10 <170> SOFTWARE: PatentIn Ver. 2.0  
 11 <210> SEQ ID NO: 1  
 12 <211> LENGTH: 1361  
 13 <212> TYPE: DNA  
 14 <213> ORGANISM: primate  
 15 <220> FEATURE:  
 16 <221> NAME/KEY: CDS  
 17 <222> LOCATION: (132)..(1061)  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: misc\_feature  
 20 <222> LOCATION: (567)  
 21 <223> OTHER INFORMATION: n at position 567; n may be A, C, G, or T;  
 22 translated amino acid depends on genetic code  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: misc\_feature  
 25 <222> LOCATION: (573)  
 26 <223> OTHER INFORMATION: n at position 573; n may be A, C, G, or T;  
 27 translated amino acid depends on genetic code  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: misc\_feature  
 30 <222> LOCATION: (1336)  
 31 <223> OTHER INFORMATION: n at position 1336; n may be A, C, G, or T;  
 32 translated amino acid depends on genetic code  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: misc\_feature  
 35 <222> LOCATION: (1342)  
 36 <223> OTHER INFORMATION: n at position 1342; n may be A, C, G, or T;  
 37 translated amino acid depends on genetic code  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: misc\_feature  
 40 <222> LOCATION: (1369)  
 41 <223> OTHER INFORMATION: n at position 1369; n may be A, C, G, or T;  
 42 translated amino acid depends on genetic code  
 43 <400> SEQUENCE: 1  
 44 TCGAGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGG 60  
 45 GAGAGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGG 120  
 46 GAGCGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGCGG CAGCGCGG 180  
 47 Met Glu Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr

pp 2, 3, 5

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001

TIME: 12:53:11

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\1265540C.raw

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65          1          5          10
67 aql ccl lle alq lqg lll lll lal qaa lly all ccl lql lly ccl aca 218
68 Ser leu glu Met Trp Phe Phe Tyr Ala leu lle Pro Gln leu leu Thr
69 15          20          25
71 gdl qaa qly qcc ser alq ccl qcc ccl cag aac ccl lcl qaa ccl lea 266
72 Asp Glu Val Ala lle leu Pro Ala Pro Gln Asp leu Ser Val leu Ser
73 30          35          40          45
75 aca aca arg aca ccl lle lly alq lly lly qcc cca qly aca qcc ccl qaa 311
76 Thr Arg Met Lys His leu leu Met Trp Ser Pro Val lle Ala Pro Gly
77 50          55          60
79 qaa aca qly lal lal lal glc qaa lal cag qaa qaa lal qaa qaa qly 367
80 Glu Thr Val Tyr Trp Ser Val Glu Tyr Glu Glu Glu Tyr Glu Ser leu
81 65          70          75
83 lal aca qcc ccl aca aca lly aca ccl qcc aca lly lly leu ccl aca qaa 419
84 Trp Thr Ser His lle Trp lle Pro Ser Ser Trp Gln Ser leu Thr Glu
85 80          85          90
87 qql ccl qag lly qaa qaa aca qcc qaa qaa aca qcc aca qly cca lal 465
88 Gly Pro Glu Cys Asp Val Thr Asp Asp lle Thr Ala Thr Val Pro Tyr
89 95          100          105
91 aca ccl ccl glc qaa qcc aca lly qaa lea qaa aca lea qaa lly qaa 500
92 Asn leu Asn Val Arg Ala Thr leu Gly Ser Glu Thr Ser Ala Trp Ser
93 110          115          120          125
95 aca cca qaa ccl ccl ccl aca qaa qaa lea aca aca ccl aca qaa ccl 554
96 lle leu cca His Pro Phe Asn Arg Asn Ser Thr lle leu Thr Ala Pro
97 130          135          140
99 gaa aca qaa aca aca aca qcc ccl ccl ccl ccl ccl att gag cly gag 602
100 Gly Met Glu Ile (Xaa) Lys (Xaa) Gly Phe His leu Val lle Glu leu Glu
101 145          150          155
103 qaa cly qaa qcc cca lly qaa lly ccl qaa qcc lal cag aca qaa qaa 650
104 Asp leu Gly Pro Gln Phe Glu Phe leu Val Ala Tyr Trp Xaa Arg Glu
105 160          165          170
107 ccl qcc qcc qaa qaa ccl qcc aca aca qaa qaa qaa qaa qaa qaa 698
108 Pro Gly Ala Glu Glu Ala Val Lys Met Val Arg Ser Gly Gly lle Pro
109 175          180          185
111 qly cca cca qaa aca arg qaa cca qaa qaa qaa qaa lal lyl qly aca qcc 746
112 Val His leu Glu Thr Met Glu Pro Gly Ala Ala Thr Cys Val Lys Ala
113 190          195          200          205
115 aca aca lly qly aca qcc att qaa arg lly qcc qcc lle aca qaa aca 791
116 Glu Thr Phe Val Lys Ala lle Gly Xaa Tyr Ser Ala Phe Ser Glu Thr
117 210          215          220
119 qaa lal qly qaa qaa qaa qaa qaa qcc att cca cly qaa cly qcc qly 817
120 Glu Cys Val Xaa Val Gln Gly Glu Ala lle Pro leu Val leu Ala leu
121 225          230          235
123 lly qcc lly qly qcc lly aca qaa qaa aca ccl qly glc qly cca arg lle 860
124 Phe Ala Phe Val Gly Phe Met leu lle leu Val Val Val Pro leu Phe
125 240          245          250
127 qcc qaa aca arg qcc qaa cly cca cca lal ccc lyl ccc ccc qly qly 938
128 Val Trp Lys Met Gly Arg leu leu Glu Tyr Ser Cys Cys Pro Val Val
129 255          260          265

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*Please align amino acids directly under corresponding codon.*

## RAW SEQUENCE LISTING

PATIENT APPLICATION: US/02/265,540C

DATE: 01/07/2001

TIME: 12:53:11

Input Seq: A:\804k.app

Output Seq: M:\CRF3\01022001\I265540C.raw

141 ggc ctc cta gac acc tgg aca aca gac gac leu cgc gac aac gta atc 986  
142 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
143 270 275 300 305  
144 ggc ctc cta gac acc tgg aca aca gac gac leu cgc gac aac gta atc 1031  
145 Ser Cys Arg Arg Gln Val Asp Ala Cys Ala Thr Ala Val Met Ser  
146 290 295 300  
147 cct gac gac ctc ctc aat gac tgg atc tgg tgggttggc gagggttggc 1084  
148 Pro Gln Gln Leu Leu Arg Ala Trp Ile Ser  
149 305 310  
150 ggttgggtggc ggttgggtggc cgttgggtggc ggttgggtggc ggttgggtggc 1141  
151 ggttgggtggc ggttgggtggc ggttgggtggc ggttgggtggc ggttgggtggc 1201  
152 ggttgggtggc ggttgggtggc ggttgggtggc ggttgggtggc ggttgggtggc 1261  
153 ggttgggtggc ggttgggtggc ggttgggtggc ggttgggtggc ggttgggtggc 1321  
154 cttcttcttctt tgggttcttctt gtttcttctt ctgttcttctt ggttcttcttctt 1381  
155 2102 SEQ ID NO: 2  
156 2112 LENGTH: 311  
157 2122 TYPE: CDP  
158 2132 ORIGIN: primate  
159 2142 SEQUENCE: 2  
160 Met Gln Thr Phe Thr Met Val Leu Gln Gln Ile Trp Thr Ser Leu Phe  
161 1 5 10 15  
162 Met Trp Phe Phe Tyr Ala Leu Ile Pro Lys Leu Leu Thr Asp Gln Val  
163 20 25 30  
164 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met  
165 35 40 45  
166 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Phe Gly Gln Thr Val  
167 50 55 60  
168 Tyr Tyr Ser Val Gln Tyr Gln Gly Gln Tyr Gln Ser Leu Tyr Thr Ser  
169 65 70 75 80  
170 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Gln Gly Pro Gln  
171 85 90 95  
172 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Leu Tyr Leu Leu Arg  
173 100 105 110  
174 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
175 115 120 125  
176 His Pro Phe Asn Arg Asn Ser Thr Thr Leu Thr Arg Pro Gly Met Gln  
177 130 135 140  
W--> 187 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Gln Leu Glu Asp Leu Gly  
188 145 150 155 160  
W--> 190 Pro Gln Phe Gln Thr Leu Val Ala Tyr Trp Xaa Arg Gln Pro Gly Ala  
191 165 170 175  
192 Gln Gln His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu  
193 180 185 190  
194 Gln Thr Met Gln Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe  
195 195 200 205  
W--> 199 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Gln Cys Val  
200 210 215 220  
W--> 202 Xaa Val Gln Gly Gln Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
203 225 230 235 240

See item 10 on  
Error Summary  
Sheet



## 12.341 93/94/9501

7 (HV): 12:59:10

Output: S:\C:\N:\CRE3\01023001\1265540C.rdw

OK

## REV: 01/01/2001

919b. 12:54:41

Output Set: X:\CRF3\01022001\I263540C.rnw

[illegible]

10

## VERIFICATION SUMMARY

DATE: 01/02/2001

PATENT APPLICATION: US/02/265,540C

FILE: 125540C

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\I265540C.raw

L:100 H:141 W: (46) "n" or "Xaa" used, for SEQ 104:1  
 L:100 H:141 W: (46) "n" or "Xaa" used, for SEQ 104:1  
 L:104 H:141 W: (46) "n" or "Xaa" used, for SEQ 104:1  
 L:116 H:141 W: (46) "n" or "Xaa" used, for SEQ 104:1  
 L:120 H:141 W: (46) "n" or "Xaa" used, for SEQ 104:1  
 L:151 H:141 W: (46) "n" or "Xaa" used, for SEQ 104:1  
 L:157 H:158 W: Mandatory Feature missing, +220 not found for SEQ 104:2  
 L:167 H:158 W: Mandatory Feature missing, +221 not found for SEQ 104:2  
 L:167 H:158 W: Mandatory Feature missing, +222 not found for SEQ 104:2  
 L:167 H:158 W: Mandatory Feature missing, +223 not found for SEQ 104:2  
 L:167 H:140 W: (46) "n" or "Xaa" used: Feature required, for SEQ 104:2  
 L:190 H:158 W: Mandatory Feature missing, +220 not found for SEQ 104:2  
 L:190 H:158 W: Mandatory Feature missing, +221 not found for SEQ 104:2  
 L:190 H:158 W: Mandatory Feature missing, +222 not found for SEQ 104:2  
 L:190 H:158 W: Mandatory Feature missing, +223 not found for SEQ 104:2  
 L:190 Repeated in SeqNo2  
 L:199 H:158 W: Mandatory Feature missing, +220 not found for SEQ 104:2  
 L:199 H:158 W: Mandatory Feature missing, +221 not found for SEQ 104:2  
 L:199 H:158 W: Mandatory Feature missing, +222 not found for SEQ 104:2  
 L:199 H:158 W: Mandatory Feature missing, +223 not found for SEQ 104:2  
 L:202 H:158 W: Mandatory Feature missing, +220 not found for SEQ 104:2  
 L:202 H:158 W: Mandatory Feature missing, +221 not found for SEQ 104:2  
 L:202 H:158 W: Mandatory Feature missing, +222 not found for SEQ 104:2  
 L:202 H:158 W: Mandatory Feature missing, +223 not found for SEQ 104:2  
 L:204 H:158 W: Mandatory Feature missing, +223 not found for SEQ 104:3  
 L:214 H:140 W: (46) "n" or "Xaa" used: Feature required, for SEQ 104:3  
 L:125 H:158 W: Mandatory Feature missing, +220 not found for SEQ 104:4  
 L:125 H:158 W: Mandatory Feature missing, +221 not found for SEQ 104:4  
 L:125 H:158 W: Mandatory Feature missing, +222 not found for SEQ 104:4  
 L:125 H:158 W: Mandatory Feature missing, +223 not found for SEQ 104:4  
 L:125 H:140 W: (46) "n" or "Xaa" used: Feature required, for SEQ 104:4

No  
 X  
 X